



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/980,468

DATE: 05/15/2002

TIME: 13:51:33

Input Set : A:\980468

Output Set: N:\CRF3\05152002\I980468.raw

ENTERED

4 <110> APPLICANT: BASF Aktiengesellschaft  
7 <120> TITLE OF INVENTION: D6 acetylenase and D6 desaturase from Ceratodon purpureus  
9 <130> FILE REFERENCE: 99 1388  
11 <140> CURRENT APPLICATION NUMBER: US 09/980,468  
12 <141> CURRENT FILING DATE: 2002-12-03  
14 <150> PRIOR APPLICATION NUMBER: 19925718.3  
15 <151> PRIOR FILING DATE: 1999-06-07  
17 <160> NUMBER OF SEQ ID NOS: 28  
19 <170> SOFTWARE: PatentIn Vers. 2.0  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 2040  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Ceratodon purpureus  
26 <220> FEATURE:  
27 <221> NAME/KEY: CDS  
28 <222> LOCATION: (176)..(1627)  
30 <400> SEQUENCE: 1  
32 ctcaggcagg tctcagttga tgagacgctg agttctgaat cctttgagct gtgtcaggct 60  
34 cggcacttgt gggatggtga aggagtgatc gatcaggagt gcaggagctg cattagtttc 120  
36 tcaggggtcga tcagggttatt ctgaaaaagg ctgcgtctgt gagcagtttg caaaa atg 178  
37 Met  
38 1  
40 gcc ctc gtt acc gac ttt ctg aac ttt ctg ggc acg aca tgg agc aag 226  
41 Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser Lys  
42 5 10 15  
44 tac agc gtg tac acc cat agc tat gct gga aac tat ggg cct act ttg 274  
45 Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr Leu  
46 20 25 30  
48 aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg gga cag aca 322  
49 Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln Thr  
50 35 40 45  
52 ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act tac tct ctg 370  
53 Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser Leu  
54 50 55 60 65  
56 gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg atg atc gtc 418  
57 Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile Val  
58 70 75 80  
60 aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac cac cct gga 466  
61 Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro Gly  
62 85 90 95  
64 ggg acg gta att agc acc tac ttt ggg cgg gat ggc aca gac gtt ttc 514  
65 Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe  
66 100 105 110

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68 gca aca ttc cat cca cct gcc gca tgg aag caa ctc aat gac tac tac 562
69 Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn Asp Tyr Tyr
70 115 120 125
72 att gga gac ctt gct agg gaa gag ccc ctt gat gaa ttg ctt aaa gac 610
73 Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu Leu Lys Asp
74 130 135 140 145
76 tac aga gat atg aga gcc gag ttt gtt aga gaa ggg ctt ttc aag agt 658
77 Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu Phe Lys Ser
78 150 155 160
80 tcc aag gcc tgg ttc ctg ctt cag act ctg att aat gca gct ctc ttt 706
81 Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala Ala Leu Phe
82 165 170 175
84 gct gcg agc att gcg act atc tgt tac gac aag agt tac tgg gct att 754
85 Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr Trp Ala Ile
86 180 185 190
88 gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag tgt gga tgg 802
89 Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly Trp
90 195 200 205
92 ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac cgt acc gcg 850
93 Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr Ala
94 210 215 220 225
96 aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt ggc ttt agt 898
97 Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe Ser
98 230 235 240
100 gta tca tgg tgg agg acg aag cac aac att cat cat act gct ccg aat 946
101 Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro Asn
102 245 250 255
104 gag tgc gac gaa cag tac aca cct cta gac gaa gac att gat act ctc 994
105 Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile Asp Thr Leu
106 260 265 270
108 ccc atc att gcc tgg agc aag gaa att ttg gcc acc gtt gag agc aag 1042
109 Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val Glu Ser Lys
110 275 280 285
112 aga att ttg cga gtg ctt caa tat cag cac tac atg att ctg cct cta 1090
113 Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile Leu Pro Leu
114 290 295 300 305
116 ttg ttc atg gcc cgg tac agt tgg act ttt gga agt ttg ctc ttc aca 1138
117 Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu Leu Phe Thr
118 310 315 320
120 ttc aat cct gat ttg agc acg acc aag gga ttg ata gag aag gga aca 1186
121 Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu Lys Gly Thr
122 325 330 335
124 gtt gct ttt cac tac gcc tgg ttc agt tgg gct gcg ttc cat att ttg 1234
125 Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe His Ile Leu
126 340 345 350
128 ccg ggt gtc gct aag cct ctt gcg tgg atg gta gca act gag ctt gtg 1282
129 Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr Glu Leu Val
130 355 360 365
132 gcc ggt ttg ttg ttg gga ttc gtg ttt acg ttg agt cac aat gga aag 1330

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133 Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly Lys
134 370          375          380          385
136 gag gtt tac aat gaa tcg aag gac ttc gtg aga gcc cag gtt att acc 1378
137 Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile Thr
138          390          395          400
140 acc cgt aac acc aag cga ggc tgg ttc aac gat tgg ttc act ggg gga 1426
141 Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly Gly
142          405          410          415
144 ctc gac acc cag att gag cat cac ctg ttt cca aca atg ccc agg cac 1474
145 Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His
146          420          425          430
148 aac tac ccc aag atc gca cct cag gtc gag gct ctt tgc aag aag cac 1522
149 Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys His
150          435          440          445
152 ggc ctc gag tac gat aat gtc tcc gtc gtt ggt gcc tct gtc gcg gtt 1570
153 Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala Val
154 450          455          460          465
156 gtg aag gcg ctc aag gaa att gct gat gaa gcg tca att cgg ctt cac 1618
157 Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu His
158          470          475          480
160 gct cac taa gaaatcgtcg aactttgact attcattttt ttgcctggc 1667
161 Ala His
163 tacctcaaat gttcgggagc aggtgcttgg cagtgtgttc aaccggagcg cactgaaaat 1727
165 gtgcagaatc catttccaga aattaccatt cctagctaaa tcttcttttt accaggtcgg 1787
167 atatatgaaa cttttttgat gcaacaagta gcattcaatt gaagacattg ttcgagatat 1847
169 aattcgcagt gtttctattc agcgggcata cgtactagtc catatcggcg gttgccgaga 1907
171 gtttacatta ttagttggca caacgagtag atctagtgtg aatttctatt tccgcagtga 1967
173 atattactct gaatatatac cgttatctat tttcctaaaa aaaaaaaaaa aaaaaaaaaa 2027
175 aaaaaaaaaa aaa 2040
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 483
180 <212> TYPE: PRT
181 <213> ORGANISM: Ceratodon purpureus
183 <400> SEQUENCE: 2
185 Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser
186 1 5 10 15
188 Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr
189 20 25 30
191 Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln
192 35 40 45
194 Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser
195 50 55 60
197 Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile
198 65 70 75 80
200 Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro
201 85 90 95
203 Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val
204 100 105 110
206 Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn Asp Tyr

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207          115          120          125
209 Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu Leu Lys
210          130          135          140
212 Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu Phe Lys
213 145          150          155          160
215 Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala Ala Leu
216          165          170          175
218 Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr Trp Ala
219          180          185          190
221 Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly
222          195          200          205
224 Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr
225          210          215          220
227 Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe
228 225          230          235          240
230 Ser Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro
231          245          250          255
233 Asn Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile Asp Thr
234          260          265          270
236 Leu Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val Glu Ser
237          275          280          285
239 Lys Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile Leu Pro
240          290          295          300
242 Leu Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu Leu Phe
243 305          310          315          320
245 Thr Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu Lys Gly
246          325          330          335
248 Thr Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe His Ile
249          340          345          350
251 Leu Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr Glu Leu
252          355          360          365
254 Val Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly
255          370          375          380
257 Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile
258 385          390          395          400
260 Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly
261          405          410          415
263 Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg
264          420          425          430
266 His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys
267          435          440          445
269 His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala
270          450          455          460
272 Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu
273 465          470          475          480
275 His Ala His
278 <210> SEQ ID NO: 3
279 <211> LENGTH: 1467
280 <212> TYPE: DNA

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281 <213> ORGANISM: Ceratodon purpureus
283 <220> FEATURE:
284 <221> NAME/KEY: CDS
285 <222> LOCATION: (10)..(1461)
287 <400> SEQUENCE: 3
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290      Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr
291      1          5          10
293 tgg agc aag tac agc gtg tac acc cat agc tat gct gga aac tat ggg 99
294 Trp Ser Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly
295 15          20          25          30
297 cct act ttg aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg 147
298 Pro Thr Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala
299      35          40          45
301 gga cag aca ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act 195
302 Gly Gln Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr
303      50          55          60
305 tac tct ctg gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg 243
306 Tyr Ser Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp
307      65          70          75
309 atg atc gtc aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac 291
310 Met Ile Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp
311      80          85          90
313 cac cct gga ggg acg gta att agc acc tac ttt ggg cgg gat ggc aca 339
314 His Pro Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr
315 95          100          105          110
317 gac gtt ttc gca aca ttc cat cca cct gcc gca tgg aag caa ctc aat 387
318 Asp Val Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn
319      115          120          125
321 gac tac tac att gga gac ctt gct agg gaa gag ccc ctt gat gaa ttg 435
322 Asp Tyr Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu
323      130          135          140
325 ctt aaa gac tac aga gat atg aga gcc gag ttt gtt aga gaa ggg ctt 483
326 Leu Lys Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu
327      145          150          155
329 ttc aag agt tcc aag gcc tgg ttc ctg ctt cag act ctg att aat gca 531
330 Phe Lys Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala
331      160          165          170
333 gct ctc ttt gct gcg agc att gcg act atc tgt tac gac aag agt tac 579
334 Ala Leu Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr
335 175          180          185          190
337 tgg gct att gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag 627
338 Trp Ala Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln
339      195          200          205
341 tgt gga tgg ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac 675
342 Cys Gly Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn
343      210          215          220
345 cgt acc gcg aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt 723
346 Arg Thr Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 15  
Seq#:14; N Pos. 3,12,15  
Seq#:15; N Pos. 3,6,12